

- 63 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Levy, Gary
- (ii) TITLE OF INVENTION: Methods of Modulating Immune Coagulation
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BERESKIN & PARR
 - (B) STREET: 40 King Street West
 - (C) CITY: Toronto
 - (D) STATE: Ontario
 - (E) COUNTRY: Canada
 - (F) ZIP: M5H 3Y3
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Gravelle, Micheline
 - (B) REGISTRATION NUMBER: 40,261
 - (C) REFERENCE/DOCKET NUMBER: 9579-006
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (416) 364-7311
 - (B) TELEFAX: (416) 361-1398

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATCTAGGGT TGGAAGCCAG GTCTCCTGAG TATGCGAGAA TAAATACAGT CATGGAAGTG	60
TAAAGAGTCT GCCAACATTT TGAGAATGTG AATAGGATTT GGCTAAAATT AAGGGGATAT	120
ACAGAAAAGT CATAGGAAAT CAGGTTAAAG ACATAAATAT GAGATAGGCT ACAGAGTGTT	180
TTAAGTAATA CAATAAACA TTTAGATTTT TGCCCATGTC AGTCATTTTG AAATTATTTT	240
TAAAGCAAAA AAACCTTTT TAAACAAGAA ATCTTATGAG ATGTCAATAT GCAAAACAAA	300
TTAAAAGGAG GTGGTTTCTC TAACTGAAGC TGTTCTCTT TCCTGCCTTC AGCCTCTGAA	360

GAGAAAGTTA	GAAAACTATT	ATCATTAATG	CTACATGTTT	TGAACAAGCT	GATATACCAA	420
GTGGCCCAGA	GAGCAGGTAG	AAGAACCAGC	GTGGAGACAG	AAAGCAAGAG	GCCCCCCTGC	480
CAGGGCTACC	TGCAGAAAAG	AAGGGCAAAG	ATGCTGTAGG	CAAGAGAAGT	TCAGGACAGA	540
CACTGGCATA	GCTCAAAGAT	TCACATTTGA	GCAGCTGTGG	AAGATGACAG	TACAATTACC	600
AAAATGTCGA	AGGGCAAAGG	AGGCAGCTAC	TGGTTTTGAT	GAAAGACAAT	TATGTCCTTT	660
TAAATGGGTC	TTAGACATTT	AGACATTTAT	ATACACTATG	CTACGGACAA	AGGAATAGAA	720
AGTAGCACTT	TTTTCTCCAC	TAGTTTTCTT	CTCTTTTTCA	AGTAGATGAA	GCAAAAGTCA	780
ACTGCAATAG	TCAGAAAAGCT	GTACTTTGTT	ACACTTAGAA	ACTTCTAAAA	GTGCTTAAGA	840
TTTCACCTGA	AAGTCCAACA	TGAAGAAAAT	ACAGGCTCCC	CAATGCCCCA	TTCTAAGAAG	900
GAAAAAGGAC	CATTTTTCATT	TTAGTAACGT	TTCTGTTCTA	TAGACAGTTT	GGATAACTAG	960
CTCTTACTTT	TTATCTTTAA	AAACTGTTTT	TCCAGTGAAG	TTACGTATAA	TTATTTACTT	1020
CAAGCGTAGT	ATACCAAATT	ACTTTAGAAA	TGCAAGACTT	TTCTTATACT	TCATAAAATA	1080
CATTATGAAA	GTGAATCTTG	TTGGCTGTGT	ACATTTGACT	ATAATAATTT	CAATGCATAT	1140
TATTTCTATT	GAGAGTAAGT	TACAGTTTTT	GGCAAACGTC	GTTTGATGAG	GGCTATCTCC	1200
TCTTCCTGTG	CGTTTCTAAA	ACTTGTGATG	CAAACGCTCC	CACCCTTTCC	TGGGAACACA	1260
GAAAGCCTGA	CTCAGGCCAT	GGCCGCTATT	AAAGCAGCTC	CAGCCCTGCG	CACTCCCTGC	1320
TGGGGTGAAG	AGCACTGTAA	AGATGAAGCT	GGCTAACTGG	TACTGGCTGA	GCTCAGCTGT	1380
TCTTGCCACT	TACGGTTTTT	TGGTTGTGGC	AAACAATGAA	ACAGAGGAAA	TTAAAGATGA	1440
AAGAGCAAAG	GATGTCTGCC	CAGTGAGACT	AGAAAGCAGA	GGGAAATGCG	AAGAGGCAGG	1500
GGAGTGCCCC	TACCAGGTAA	GCCTGCCCCC	CTTGACTATT	CAGCTCCCGA	AGCAATTCAG	1560
CAGGATCGAG	GAGGTGTTCA	AAGAAGTCCA	AAACCTCAAG	GAAATCGTAA	ATAGTCTAAA	1620
GAAATCTTGC	CAAGACTGCA	AGCTGCAGGC	TGATGACAAC	GGAGACCCAG	GCAGAAACGG	1680
ACTGTTGTTA	CCCAGTACAG	GAGCCCCGGG	AGAGGTTGGT	GATAACAGAG	TTAGAGAATT	1740
AGAGAGTGAG	GTTAACAAGC	TGTCCTCTGA	GCTAAAGAAT	GCCAAAGAGG	AGATCAATGT	1800
ACTTCATGGT	CGCCTGGAGA	AGCTGAATCT	TGTAAATATG	AACAACATAG	AAAATTATGT	1860
TGACAGCAAA	GTGGCAAATC	TAACATTTGT	TGTCAATAGT	TTGGATGGCA	AATGTTCAAA	1920
GTGTCCCAGC	CAAGAACAAA	TACAGTCACG	TCCAGGTATG	TATAATAATG	TTTTCTTATC	1980
ATATGTTTAT	AAATGTTATA	CAGTCAGAGA	TGTATCTAAA	AGATTAACTT	GAGTCAGTAA	2040
GTTAAATAGA	TGACAGATTA	AGTCTTTTAT	TTATCAAGGT	GCACAGGAAA	AAATAAATAT	2100
CTTCTCAAAT	ATGACCACAT	AAATATGACC	TAATTACAAA	ATCATAGTTA	GTTCTGTATC	2160
CACTGGAAGT	CACTTTCAAT	TTTAAGATCT	TATTTGTTAA	TGCCAGACCT	ACTTGCAAGC	2220
AGAGATTAGA	GGTCCTTTCT	GCTTTATAAC	ATTAGGTTCT	TCTTGTGAGG	CCTTAAGCAT	2280
TTACTAAACA	CCTTCAAGTA	AGTTTAGTAA	AGTTTCATTA	CTGCCATTGA	TTCAATTATC	2340

AAACTGCTTT	TGTACATATA	AAGAATTCTT	CAGATGCATG	GTTTCTATTA	ACAAGATCCA	2400
ATGCCTTCCT	TTTATTTCCC	CTTCAGTTCA	ACATCTAATA	TATAAAGATT	GCTCTGACTA	2460
CTACGCAATA	GGCAAAAGAA	GCAGTGAGAC	CTACAGAGTT	ACACCTGATC	CCAAAAATAG	2520
TAGCTTTGAA	GTTTACTGTG	ACATGGAGAC	CATGGGGGGA	GGCTGGACAG	TGCTGCAGGC	2580
ACGTCTCGAT	GGGAGCACCA	ACTTCACCAG	AACATGGCAA	GACTACAAAG	CAGGCTTTGG	2640
AAACCTCAGA	AGGGAATTTT	GGCTGGGGAA	CGATAAAATT	CATCTTCTGA	CCAAGAGTAA	2700
GGAAATGATT	CTGAGAATAG	ATCTTGAAGA	CTTTAATGGT	GTCGAACTAT	ATGCCTTGTA	2760
TGATCAGTTT	TATGTGGCTA	ATGAGTTTCT	CAAATATCGT	TTACACGTTG	GTAACATATA	2820
TGGCACAGCT	GGAGATGCAT	TACGTTTCAA	CAAACATTAC	AACCACGATC	TGAAGTTTTT	2880
CACCACTCCA	GATAAAGACA	ATGATCGATA	TCCTTCTGGG	AACTGTGGGC	TGTACTACAG	2940
TTCAGGCTGG	TGGTTTGATG	CATGTCTTTC	TGCAAACTTA	AATGGCAAAT	ATTATCACCA	3000
AAAATACAGA	GGTGTCCGTA	ATGGGATTTT	CTGGGGTACC	TGGCCTGGTG	TAAGTGAGGC	3060
ACACCCTGGT	GGCTACAAGT	CCTCCTTCAA	AGAGGCTAAG	ATGATGATCA	GACCCAAGCA	3120
CTTTAAGCCA	TAAATCACTC	TGTTCAATTCC	TCCAGGTATT	CGTTATCTAA	TAGGGCAATT	3180
AATTCCTTGT	TTCATATTTT	TCATAGCTAA	AAAATGATGT	CTGACGGCTA	GGTTCTTATG	3240
CTACACAGCA	TTTGAAATAA	AGCTGAAAAA	CAATGCATTT	TAAAGGAGTC	CTTTGTTGTT	3300
ATGCTGTTAT	CCAATGAACA	CTTGCAAGCA	ATTAGCAATA	TTGAGAATTA	TACATTAGAT	3360
TTACAATTCT	TTTAATTTCT	ATTGAAACTT	TTTCTATTGC	TTGTATTACT	TGCTGTATTT	3420
AAAAAATAAT	TGTTGGCTGG	GTGTGGTAGC	TCACGCCTGT	AATCCCAGCA	CTTTGGAATG	3480
TCAAGGCAGG	CAGATCACTT	GAGGTCAGGA	GTTTGAGACC	AGCCTGGCCA	AACATGTGAA	3540
ACGCTGTCTC	TATTAAAAAT	ACAAAAATTA	GCCGGGCATG	GTGGTACATG	CCTGTAATCA	3600
ACGCTGTTTA	TTAAAAATAC	AAAAATTAGC	CGGGCATGGT	GGACATGCCT	GTAATCCTAG	3660
TACTTGGGAG	GCTGAGGCAG	GAGAATCGCT	TGAACCTGAG	AGGAAGAGGT	TGCAGTGAGC	3720
CAAGAATGAG	CCACTGCACT	CCAGCATGGG	TGACAGAGAA	AACTCTGTCT	CAAACAAAAA	3780
AATAATAAAA	TTTATTCAGT	AGGTGGATTC	TACACAAAGT	AATCTGTATT	TGGGCCATGA	3840
TTTAAGCACA	TCTGAAGGTA	TATCACTCTT	TTCAGGCTAT	AATTATTTGG	GTAATCTTCA	3900
TTCTGAGACA	AACTTAATCT	ATATCATTTA	CTTTGCAACA	GAACAACCCT	ACAGCATTTT	3960
GGTCCCAGA	CTAAGGGAAC	TAATATCTAT	ATAATTAAAC	TTGTTCAATTT	ATCATTCATG	4020
AAATATAAAA	TACTTGTCAT	TTAAACCGTT	TAAAAATGTG	GTAGCATAAT	GTCACCCCAA	4080
AAAGCATTCA	GAAAGCAATG	TAAGTGTGAA	GACCAGGGTT	TAAAGGTAAT	TCATTTATAG	4140
TTTATAACTC	CTTAGATGTT	TGATGTTGAA	AACTGCTTTA	ACATGAAAAAT	TATCTTCCTC	4200
TGCTCTGTGT	GAACAATAGC	TTTTAATTTA	AGATTGCTCA	CTACTGTACT	AGACTACTGG	4260
TAGGTTTTTTT	TGGGGGGGGG	TGGGTAGGGA	TATGTGGGTA	ATGAAGCATT	TACTTACAGG	4320

(2) INFORMATION FOR SEQ ID NO:2:

(A) LENGTH: 439 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:2:

Met 1	Lys	Leu	Ala	Asn 5	Trp	Tyr	Trp	Leu	Ser 10	Ser	Ala	Val	Leu	Ala 15	Thr
Tyr	Gly	Phe	Leu 20	Val	Val	Ala	Asn	Asn 25	Glu	Thr	Glu	Glu	Ile 30	Lys	Asp
Glu	Arg	Ala 35	Lys	Asp	Val	Cys	Pro 40	Val	Arg	Leu	Glu	Ser 45	Arg	Gly	Lys
Cys	Glu 50	Glu	Ala	Gly	Glu	Cys 55	Pro	Tyr	Gln	Val	Ser 60	Leu	Pro	Pro	Leu
Thr 65	Ile	Gln	Leu	Pro	Lys 70	Gln	Phe	Ser	Arg	Ile 75	Glu	Glu	Val	Phe	Lys 80
Glu	Val	Gln	Asn 85	Leu	Lys	Glu	Ile	Val	Asn 90	Ser	Leu	Lys	Lys	Ser 95	Cys
Gln	Asp	Cys	Lys 100	Leu	Gln	Ala	Asp	Asp 105	Asn	Gly	Asp	Pro	Gly 110	Arg	Asn
Gly	Leu 115	Leu	Leu	Pro	Ser	Thr	Gly 120	Ala	Pro	Gly	Glu	Val 125	Gly	Asp	Asn
Arg 130	Val	Arg	Glu	Leu	Glu	Ser 135	Glu	Val	Asn	Lys	Leu 140	Ser	Ser	Glu	Leu
Lys 145	Asn	Ala	Lys	Glu	Glu 150	Ile	Asn	Val	Leu	His 155	Gly	Arg	Leu	Glu	Lys 160
Leu	Asn	Leu	Val 165	Asn	Met	Asn	Asn	Ile	Glu 170	Asn	Tyr	Val	Asp	Ser 175	Lys
Val	Ala	Asn 180	Leu	Thr	Phe	Val	Val	Asn 185	Ser	Leu	Asp	Gly	Lys 190	Cys	Ser
Lys	Cys	Pro 195	Ser	Gln	Glu	Gln	Ile 200	Gln	Ser	Arg	Pro	Val 205	Gln	His	Leu
Ile 210	Tyr	Lys	Asp	Cys	Ser	Asp 215	Tyr	Tyr	Ala	Ile	Gly 220	Lys	Arg	Ser	Ser

- 67 -

Glu Thr Tyr Arg Val Thr Pro Asp Pro Lys Asn Ser Ser Phe Glu Val
 225 230 235 240
 Tyr Cys Asp Met Glu Thr Met Gly Gly Gly Trp Thr Val Leu Gln Ala
 245 250 255
 Arg Leu Asp Gly Ser Thr Asn Phe Thr Arg Thr Trp Gln Asp Tyr Lys
 260 265 270
 Ala Gly Phe Gly Asn Leu Arg Arg Glu Phe Trp Leu Gly Asn Asp Lys
 275 280 285
 Ile His Leu Leu Thr Lys Ser Lys Glu Met Ile Leu Arg Ile Asp Leu
 290 295 300
 Glu Asp Phe Asn Gly Val Glu Leu Tyr Ala Leu Tyr Asp Gln Phe Tyr
 305 310 315 320
 Val Ala Asn Glu Phe Leu Lys Tyr Arg Leu His Val Gly Asn Tyr Asn
 325 330 335
 Gly Thr Ala Gly Asp Ala Leu Arg Phe Asn Lys His Tyr Asn His Asp
 340 345 350
 Leu Lys Phe Phe Thr Thr Pro Asp Lys Asp Asn Asp Arg Tyr Pro Ser
 355 360 365
 Gly Asn Cys Gly Leu Tyr Tyr Ser Ser Gly Trp Trp Phe Asp Ala Cys
 370 375 380
 Leu Ser Ala Asn Leu Asn Gly Lys Tyr Tyr His Gln Lys Tyr Arg Gly
 385 390 395 400
 Val Arg Asn Gly Ile Phe Trp Gly Thr Trp Pro Gly Val Ser Glu Ala
 405 410 415
 His Pro Gly Gly Tyr Lys Ser Ser Phe Lys Glu Ala Lys Met Met Ile
 420 425 430
 Arg Pro Lys His Phe Lys Pro
 435

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATAAGGCGT GTCTGACAAA TTCTTCATAC ACACATTTCC CCTTTGCACA TTCAGTCTGT	60
ATAGGTTATT TCTATAGGAG AAAAAAATA TTCAAATTCC TTGTGCACTG GTAACAGGCA	120
TGAAGGCTCA GCAAAGCCAA TACGTGTTAT GTCCAGTTGG AGACAGTGCC AGGGCCAACA	180
TTCCAGACTT CTCAGATAGA AAGTGCGCCT GCCTGCCCTG CTCTGAGAAT TTGAAGAGAG	240
TAGTTCA GTT AGAATTAAGA GGCAGTAGAG AAAAGTCTTG GGAAATCTGG TTAGAGATAT	300
AAATATGAGA ACTGGACATG GTGGTACACA CCTGTGATCT CTGTGTTTAG GAGGGAGAGG	360

CTCTCTCTTC	TCTCTCTCTC	TCTCTCTCTC	TCTCTCTCTC	TCTCTCTCTC	TCTCTCTCTC	2400
CTCCCTCCCT	CCCTCTCTCT	CTCTTTGTGT	GCGTGTGTGG	TGGGGATGAG	GACACGTGTA	2460
GAACTTCGGG	GGTTGAGACT	TAGTGCATAT	GCATCCTCAC	CATTCCAGTT	AGTGAATGTT	2520
AACACTATTT	AAGGTCACAG	ACCTAACAGC	CTTCTGTGTC	CGGATTCCTG	GATTCCCTAGG	2580
ACCTTTGTGG	ATGGGTGGCC	ACACCCCTCTG	TGTTTCATCCT	GACTGTGAGG	TCGATGGGAC	2640
ATAGTAGGGA	TAACTTTCAT	TTGGAATCTC	TAGAGATGGT	AGGTCATCAT	GTCATAGAAT	2700
GTTATCACTA	ATGACCAAGA	TAGACACTCA	TGTTTAAGAG	ACATCACAAG	GTGTATATTA	2760
AATATGACAT	GGCATATAAC	TTGTAATGAC	ACAAAAATAT	TCTGTTACCT	ACTTTTCTCC	2820
TAAAAGCTTG	GGACTCTCCA	GAGTTCTAAA	TACATGCAAA	CAGATTATTG	TGTTTTACAG	2880
GAATCTTATA	TTGAACTTTC	TTTACCTGAC	TCAAATTTTA	TTAAAATTAA	CTGGGAACAA	2940
ATAGTTGGTC	TCTAATCTCT	ACAAAAACCA	CCAAATGATT	AACTGAGCA	TAATTATAAT	3000
CACCCTGCTG	CTACGTCTAG	AAACCAAAC	GTGAAATATT	GGCTGACTGT	ATACCTTCCT	3060
AAATAATAAA	TTCAGGATAA	CATTGCCATA	TTATTGGAGA	ACCCCCCT	CCCTTTTAAA	3120
ACTGGAATCA	TTTTATGTCA	ATCTCAGGTG	AAATACGAAT	GGGTTTCAGA	ACAGTGCTGT	3180
GCACTGAAGG	CTGACATTTA	GAACATATAT	AACGATTTCT	GTAAAGTCTG	CTGTAACAAT	3240
TGCTGATTGT	ATCCTAGGAG	ACTTGGACTC	CTCTCAACGT	TAAGGCAGAG	GAATATAATG	3300
GTTATGAGAG	TAAAACCTCT	TGTCAGGTAC	ATCTGGCTTT	CTGTCCCAGC	TCTGTCACTT	3360
AACACTTAGT	TGCGGTGGGA	AACTCCCTG	ATCTTCCGGG	AGACTAAGTA	ACTGTATAAG	3420
CAAGCTGGCC	GTGATATCCA	CGTCGTAAGG	CTGCTGTGTG	GGTTCAGTGA	AACTGTTC	3480
AGTGATTGGC	AGAGTTTCTG	GAGGTCATTG	ACCCTCATTA	AACCTTGCAT	AACTTATTC	3540
TTACTACTCT	TTGCTGTTAG	TGTTGCCACC	AGGATTGCCA	TTCAAGGCAG	TCCTGTATAC	3600
TTGATAACAC	CAGTTGGTTC	TGAGGCCCTTA	GTTAGCATCT	GTTAGCCTGG	TTCAGGAGAG	3660
TGTATCAGAG	CCAGGTTCCCT	CTATCACATA	AACTGTAACG	CAAGTGAATT	GTCCAATTGC	3720
TGTTGAGTCT	GAGAGTCCTT	GAGGTGCATA	GCTTTGACTA	ATAAATCCCC	ATGCTTTTAT	3780
GCTTTTCCTT	CCTCCCTCTT	CCAGTTCAAC	ATCTAATATA	CAAAGATTGT	TCCGACCACT	3840
ACGTGCTAGG	AAGGAGAAGC	AGTGGGGCCT	ACAGAGTTAC	CCCTGATCAC	AGAAACAGCA	3900
GCTTTGAGGT	CTACTGTGAC	ATGGAGACCA	TGGGTGGAGG	CTGGACGGTG	CTGCAGGCTC	3960
GCCTTGATGG	CAGCACCAAC	TTCACCAGAG	AGTGGAAGA	CTACAAAGCC	GGCTTTGGAA	4020
ACCTTGAACG	AGAATTTTGG	TTGGGCAACG	ATAAAATTCA	TCTTCTGACC	AAGAGTAAGG	4080
AAATGATTTT	GAGAATAGAT	CTTGAAGACT	TTAATGGTCT	CACACTTTAT	GCCTTGATG	4140
ATCAGTTTTA	TGTGGCTAAT	GAATTTCTCA	AATACCGATT	ACACATCGGT	AACTACAATG	4200
GCACGGCAGG	GGATGCCTTG	CGTTTCAGTC	GACACTACAA	CCATGACCTG	AGGTTTTTCA	4260
CAACCCAGAG	CAGAGACAAC	GATCGGTACC	CCTCTGGGAA	CTGTGGGCTC	TATTACAGCT	4320

- 70 -

CAGGCTGGTG GTTTGATTCA TGTCTCTCTG CCAATTTAAA TGGCAAATAT TACCACCAGA 4380
 AATACAAAGG TGTCCGTAAT GGGATTTTCT GGGGCACCTG GCCTGGTATA AACCAGGCAC 4440
 AGCCAGGTGG CTACAAGTCC TCCTTCAAAC AGGCCAAGAT GATGATTAGG CCCAAGAATT 4500
 TCAAGCCATA AATTGCTAGT GTTCATCTCT CTGGGCACTC ACTATCTAAG AGGACGATGA 4560
 ATTCCTTCAG CCCTTTACCA TATGTCTCAG TTTATATTCC TTTCTATGG CTAAACATTT 4620
 CCTTTAAAGC TTTACAGCTT TTAGAATAAA GCTGAAAAGA TCTAAAAAGA CTCCTATGTT 4680
 GCTGTTATAT GAGGAATGCT TGAAAGCACT GGAAATATTG ACAATTATAC ATTATAATTG 4740
 CAAAACCTTT CATTTTTATT AGTTGAAAAG TTTCTAATA TTTTATTAT TTTTATAATA 4800
 AAAACTAAAT TATTCAGCAA GCTAGATTCT ATATACGCAA GTTTTATTTT CACTAGGGCT 4860
 AAATATACAC ATTTGAGAAT ATACCAGTCC TTCCAGGTAC AACTGAAAGC CAAGAAGTGT 4920
 AGTATTATCT TTCGTCTAAG AAGAACTTAA AGCATTTTAG TTCTCAAGAA GAAGGGCAGG 4980
 GATGGGATTG GGGGCCAGGG ACAATATGTA TAGCTAAATG TATTCATCTA ATGCAAAATA 5040
 TGGCATTAAA ATACCTAAAA ATGTGGTAGC ATAATATATG TCTCTTCCCT CTCCAATTGA 5100
 AAAATAATGT TACCCTGTAG ACTTTGGTTT AGTGGTAATT CACTTACTGT TTATAGCCTG 5160
 TTAGACCGCG ATACAAAAGC TGCTTTATCC TCTCCCTCTG CTCTCTGTGC ACAATGGTTT 5220
 GTGATGTAAG GTGCTAGACT ACTGTAAGGT TTCCTTGGGG AAAGGCATGG TAAGGGAAAA 5280
 CACACTGGTT TATATTTTGA AAGCCAATCC TAATCCCCAA GCAATACTGT TGTCGAGGAG 5340
 TCAACGTTCT AGGAAGCTGA CTTTCTAGA ACAAATGTAT TTATTAGGAT GAATTGCGGA 5400
 ATT 5403

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Leu Pro Gly Trp Leu Trp Leu Ser Ser Ala Val Leu Ala Ala
 1 5 10 15
 Cys Arg Ala Val Glu Glu His Asn Leu Thr Glu Gly Leu Glu Asp Ala
 20 25 30
 Ser Ala Gln Ala Ala Cys Pro Ala Arg Leu Glu Gly Ser Gly Arg Cys
 35 40 45
 Glu Gly Ser Gln Cys Pro Phe Gln Leu Thr Leu Pro Thr Leu Thr Ile
 50 55 60
 Gln Leu Pro Arg Gln Leu Gly Ser Met Glu Glu Val Leu Lys Glu Val
 65 70 75 80

009955-0460
 002720-0950550

Arg	Thr	Leu	Lys	Glu 85	Ala	Val	Asp	Ser	Leu 90	Lys	Lys	Ser	Cys	Gln 95	Asp
Cys	Lys	Leu	Gln 100	Ala	Asp	Asp	His	Arg 105	Asp	Pro	Gly	Gly	Asn 110	Gly	Gly
Asn	Gly	Ala 115	Glu	Thr	Ala	Glu	Asp 120	Ser	Arg	Val	Gln	Glu 125	Leu	Glu	Ser
Gln	Val 130	Asn	Lys	Leu	Ser	Ser 135	Glu	Leu	Lys	Asn	Ala 140	Lys	Asp	Gln	Ile
Gln 145	Gly	Leu	Gln	Gly	Arg 150	Leu	Glu	Thr	Leu	His 155	Leu	Val	Asn	Met	Asn 160
Asn	Ile	Glu	Asn	Tyr 165	Val	Asp	Asn	Lys	Val 170	Ala	Asn	Leu	Thr	Val 175	Val
Val	Asn	Ser	Leu 180	Asp	Gly	Lys	Cys	Ser 185	Lys	Cys	Pro	Ser	Gln 190	Glu	His
Met	Gln	Ser 195	Gln	Pro	Val	Gln	His 200	Leu	Ile	Tyr	Lys	Asp 205	Cys	Ser	Asp
His	Tyr 210	Val	Leu	Gly	Arg	Arg 215	Ser	Ser	Gly	Ala	Tyr 220	Arg	Val	Thr	Pro
Asp 225	His	Arg	Asn	Ser	Ser 230	Phe	Glu	Val	Tyr	Cys 235	Asp	Met	Glu	Thr	Met 240
Gly	Gly	Gly	Trp	Thr 245	Val	Leu	Gln	Ala	Arg 250	Leu	Asp	Gly	Ser	Thr 255	Asn
Phe	Thr	Arg	Glu 260	Trp	Lys	Asp	Tyr	Lys 265	Ala	Gly	Phe	Gly	Asn 270	Leu	Glu
Arg	Glu	Phe 275	Trp	Leu	Gly	Asn	Asp 280	Lys	Ile	His	Leu	Leu 285	Thr	Lys	Ser
Lys	Glu 290	Met	Ile	Leu	Arg	Ile 295	Asp	Leu	Glu	Asp	Phe 300	Asn	Gly	Leu	Thr
Leu 305	Tyr	Ala	Leu	Tyr	Asp 310	Gln	Phe	Tyr	Val	Ala 315	Asn	Glu	Phe	Leu	Lys 320
Tyr	Arg	Leu	His	Ile 325	Gly	Asn	Tyr	Asn	Gly 330	Thr	Ala	Gly	Asp	Ala 335	Leu
Arg	Phe	Ser	Arg 340	His	Tyr	Asn	His	Asp 345	Leu	Arg	Phe	Phe 350	Thr	Thr	Pro
Asp	Arg	Asp 355	Asn	Asp	Arg	Tyr	Pro 360	Ser	Gly	Asn	Cys	Gly 365	Leu	Tyr	Tyr
Ser	Ser 370	Gly	Trp	Trp	Phe	Asp 375	Ser	Cys	Leu	Ser	Ala 380	Asn	Leu	Asn	Gly
Lys 385	Tyr	Tyr	His	Gln	Lys 390	Tyr	Lys	Gly	Val	Arg 395	Asn	Gly	Ile	Phe	Trp 400
Gly	Thr	Trp	Pro	Gly 405	Ile	Asn	Gln	Ala	Gln 410	Pro	Gly	Gly	Tyr	Lys 415	Ser
Ser	Phe	Lys	Gln 420	Ala	Lys	Met	Met	Ile 425	Arg	Pro	Lys	Asn	Phe 430	Lys	Pro

SEQUENCE LISTING



<110> Levy, Gary

<120> Methods of Modulating Immune Coagulation

<130> 9579-37

<140>

<141>

<150> US 09/442,143

<151> 1999-11-15

<160> 53

<170> PatentIn version 3.1

<210> 1

<211> 4630

<212> DNA

<213> Homo sapiens

<400> 1
gatctaggggt tggaagccag gtctcctgag tatgcgagaa taaatacagt catggaagtg 60
taaagagtct gccaacattt tgagaatgtg aataggattt ggctaaaatt aaggggatat 120
acagaaaagt cataggaaat cagggttaaag acataaatat gagataggct acagagtgtt 180
ttaagtaata caataaaaca tttagatttt tgcccatgtc agtcattttg aaattatttt 240
taaagcaaaa aaaccctttt taaacaagaa atcttatgag atgtcaatat gcaaaacaaa 300
ttaaaggag gtggtttctc taactgaagc tgttcctctt tcctgccttc agcctctgaa 360
gagaaagtta gaaaactatt atcattaatg ctacatgttt tgaacaagct gatataccaa 420
gtggcccaga gagcaggtag aagaaccagc gtggagacag aaagcaagag gcccgcctgc 480
cagggctacc tgcagaaaaga aagggcaaag atgctgtagg caagagaagt tcaggacaga 540
cactggcata gctcaaagat tcacatttga gcagctgtgg aagatgacag tacaattacc 600
aaaatgtcga agggcгааagg aggcagctac tggttttgat gaaagacaat tatgtccttt 660

taaatgggtc	ttagacattt	agacatttat	atacactatg	ctacggacaa	aggaatagaa	720
agtagcactt	ttttctccac	tagtttttctt	ctctttttca	agtagatgaa	gcaaaagtca	780
actgcaatag	tcagaaagct	gtactttgtt	acacttagaa	acttctaaaa	gtgcttaaga	840
tttcacctga	aagtccaaca	tgaagaaaat	acaggctccc	caatgccccca	ttctaagaag	900
gaaaaaggac	cattttcatt	ttagtaacgt	ttctgttcta	tagacagttt	ggataactag	960
ctcttacttt	ttatctttta	aaactgtttt	tccagtgaag	ttacgtataa	ttattttactt	1020
caagcgtagt	ataccaaatt	actttagaaa	tgcaagactt	ttcttatact	tcataaaaata	1080
cattatgaaa	gtgaatcttg	ttggctgtgt	acatttgact	ataataattt	caatgcataat	1140
tattttctatt	gagagtaagt	tacagttttt	ggcaaactgc	gtttgatgag	ggctatctcc	1200
tcttctgtg	cgttttctaaa	acttgtgatg	caaacgctcc	caccctttcc	tgggaacaca	1260
gaaagcctga	ctcaggccat	ggccgctatt	aaagcagctc	cagccctgcg	cactccctgc	1320
tggggtgagc	agcactgtaa	agatgaagct	ggctaactgg	tactggctga	gctcagctgt	1380
tcttgccact	tacggttttt	tggttgtggc	aaacaatgaa	acagaggaaa	ttaaagatga	1440
aagagcaaag	gatgtctgcc	cagtgagact	agaaagcaga	gggaaatgcg	aagaggcagg	1500
ggagtgcctc	taccaggtaa	gcctgcccc	cttgactatt	cagctcccca	agcaattcag	1560
caggatcgag	gaggtgttca	aagaagtcca	aaacctcaag	gaaatcgtaa	atagtctaaa	1620
gaaatcttgc	caagactgca	agctgcaggc	tgatgacaac	ggagaccag	gcagaaacgg	1680
actgttggtt	cccagtacag	gagccccggg	agaggttggt	gataacagag	ttagagaatt	1740
agagagttag	gttaacaagc	tgtcctctga	gctaaagaat	gccaaagagg	agatcaatgt	1800
acttcatggg	cgcctggaga	agctgaatct	tgtaaatatg	aacaacatag	aaaattatgt	1860
tgacagcaaa	gtggcaaata	taacatttgt	tgtcaatagt	ttggatggca	aatgttcaaa	1920
gtgtcccagc	caagaacaaa	tacagtcacg	tccaggtatg	tataataatg	ttttcttata	1980
atatgttcat	aaatgttata	cagtcagaga	tgtatctaaa	agattaacct	gagtcagtaa	2040
gttaaataga	tgacagatta	agtcttttat	ttatcaaggt	gcacaggaaa	aaataaatat	2100
cttctcaaat	atgaccacat	aaatatgacc	taattacaaa	atcatagtta	gttctgtatc	2160
cactggaagt	cactttcaat	tttaagatct	tatttggtta	tgccagacct	acttgcaagc	2220
agagattaga	ggtcctttct	gctttataac	attaggttct	tcttgtgagg	ccttaagcat	2280
ttactaaaca	ccttcaagta	agtttagtaa	agtttctatta	ctgccattga	ttcaattatc	2340
aaactgcttt	tgtacatata	aagaattctt	cagatgcatg	gtttctatta	acaagatcca	2400
atgccttctt	tttattttccc	cttcagttca	acatctaata	tataaagatt	gctctgacta	2460
ctacgcaata	ggcaaaaagaa	gcagtgagac	ctacagagtt	acacctgatc	ccaaaaatag	2520
tagctttgaa	gtttactgtg	acatggagac	catgggggga	ggctggacag	tgctgcaggc	2580

[illegible]

$\langle 210 \rangle$ 2

<212> PRT

 $\langle 400 \rangle$ 2

Leu Asn Leu Val Asn Met Asn Asn Ile Glu Asn Tyr Val Asp Ser Lys
165 170 175

Val	Ala	Asn	Leu	Thr	Phe	Val	Val	Asn	Ser	Leu	Asp	Gly	Lys	Cys	Ser
			180					185					190		
Lys	Cys	Pro	Ser	Gln	Glu	Gln	Ile	Gln	Ser	Arg	Pro	Val	Gln	His	Leu
		195					200					205			
Ile	Tyr	Lys	Asp	Cys	Ser	Asp	Tyr	Tyr	Ala	Ile	Gly	Lys	Arg	Ser	Ser
	210					215					220				
Glu	Thr	Tyr	Arg	Val	Thr	Pro	Asp	Pro	Lys	Asn	Ser	Ser	Phe	Glu	Val
225					230					235					240
Tyr	Cys	Asp	Met	Glu	Thr	Met	Gly	Gly	Gly	Trp	Thr	Val	Leu	Gln	Ala
				245					250					255	
Arg	Leu	Asp	Gly	Ser	Thr	Asn	Phe	Thr	Arg	Thr	Trp	Gln	Asp	Tyr	Lys
			260					265					270		
Ala	Gly	Phe	Gly	Asn	Leu	Arg	Arg	Glu	Phe	Trp	Leu	Gly	Asn	Asp	Lys
		275					280					285			
Ile	His	Leu	Leu	Thr	Lys	Ser	Lys	Glu	Met	Ile	Leu	Arg	Ile	Asp	Leu
	290					295					300				
Glu	Asp	Phe	Asn	Gly	Val	Glu	Leu	Tyr	Ala	Leu	Tyr	Asp	Gln	Phe	Tyr
305					310					315					320
Val	Ala	Asn	Glu	Phe	Leu	Lys	Tyr	Arg	Leu	His	Val	Gly	Asn	Tyr	Asn
				325					330					335	
Gly	Thr	Ala	Gly	Asp	Ala	Leu	Arg	Phe	Asn	Lys	His	Tyr	Asn	His	Asp
			340					345					350		
Leu	Lys	Phe	Phe	Thr	Thr	Pro	Asp	Lys	Asp	Asn	Asp	Arg	Tyr	Pro	Ser
		355					360					365			
Gly	Asn	Cys	Gly	Leu	Tyr	Tyr	Ser	Ser	Gly	Trp	Trp	Phe	Asp	Ala	Cys
	370					375					380				
Leu	Ser	Ala	Asn	Leu	Asn	Gly	Lys	Tyr	Tyr	His	Gln	Lys	Tyr	Arg	Gly
385					390					395					400
Val	Arg	Asn	Gly	Ile	Phe	Trp	Gly	Thr	Trp	Pro	Gly	Val	Ser	Glu	Ala
				405					410					415	
His	Pro	Gly	Gly	Tyr	Lys	Ser	Ser	Phe	Lys	Glu	Ala	Lys	Met	Met	Ile

430

cataaggcgt	gtctgacaaa	ttcttcatac	acacatttcc	cctttgcaca	ttcagttctgt	60
atagggttatt	tctataggag	aaaaaaaaata	ttcaaattcc	ttgtgcactg	gtaacaggca	120
tgaaggctca	gcaaagccaa	tacgtgttat	gtccagttgg	agacagtgcc	agggccaaca	180
ttccagactt	ctcagataga	aagtgcgcct	gcctgccctg	ctctgagaat	ttgaagagag	240
tagttcagtt	agaattaaga	ggcagtagag	aaaagtcttg	ggaaatctgg	ttagagatat	300
aaatatgaga	actggacatg	gtggtacaca	cctgtgatct	ctgtgttttag	gagggagagg	360
cagagagatc	aggagttcaa	ggccagcctg	agctacttga	gaccagttct	aaataaataa	420
gagatagatt	acagagtgcc	tttaactagt	acagagaaag	aatttggtt	tatctgtgtc	480
agttacgctg	aaataatttt	taagtaataa	aatccctttt	aataagaaac	cttatgaggt	540
cagtatgcac	aatgaactta	agagagaccc	ccagctcctg	agctgagtga	tggggaagga	600
cagccactgc	ctgtgatgtg	tgagtgacgt	gtttccaagt	gttttaacca	ctgacgatta	660
catagcctgc	acagtcagga	gaaaacagcc	gtattctctg	ccagttctct	tcctttttac	720
aaacagatga	gagacacaca	cagagaatcc	atttaaagag	cggacctttg	ttctgattag	780
gggcaatttt	aagtacttaa	gagttcacac	aaagtctagc	cttcaaaaag	aaaacaggtt	840
cccaaactag	ggaggaaaca	gaatcatttc	cattttggtg	acatttagtg	ggaagaagct	900
cacagacatt	tagacgttcc	aactctttcc	ccactagtgg	accaagtata	taatattgta	960
tcttttgggc	actggtatta	caactgtttt	ttaaacaaaa	gactttcctt	gtgctttact	1020
aaaaacccag	acggtgaatc	ttgaatacaa	tgcgtggcac	ccacggcagg	catttctattg	1080
tgcatagttt	tgactgacag	gagatgacag	catttggtctg	gctgcgcttg	ctgaggaccc	1140
tctcctcctg	tgtggcgtct	gagactgtga	tgcaaattgcg	cccgcctttt	tctgggaact	1200
cagaacgcct	gagtcaggcg	gcggtggcta	ttaaagcgcc	tggtcaggct	gggctgccgc	1260
actgcaagga	tgaggcttcc	tggttggttg	tggttgagtt	ctgccgtcct	cgctgcctgc	1320
cgagcgggtgg	aggagcacia	cctgactgag	gggctggagg	atgccagcgc	ccaggctgcc	1380

tgccccgcga	ggctggaggg	cagcgggagg	tgcgagggga	gccagtgcc	cttccagctc	1440
accctgccc	cgctgaccat	ccagctcccc	cggcagcttg	gcagcatgga	ggaggtgctc	1500
aaagaagtgc	ggaccctcaa	ggaagcagtg	gacagtctga	agaaatcctg	ccaggactgt	1560
aagttgcagg	ctgacgacca	tcgagatccc	ggcgggaatg	gagggaatgg	agcagagaca	1620
gccgaggaca	gtagagtcca	ggaactggag	agtcagggtga	acaagctgtc	ctcagagctg	1680
aagaatgcaa	aggaccagat	ccaggggctg	cagggggcgcc	tggagacgct	ccatctggta	1740
aatatgaaca	acattgagaa	ctacgtggac	aacaaagtgg	caaatctaac	cgttgtggtc	1800
aacagtttg	atggcaagtg	ttccaagtgt	cccagccaag	aacacatgca	gtcacagccg	1860
ggtaggtgta	atgaggggtca	tacagtttgt	tcatgaaagc	tgtatagcca	gatagtggcc	1920
ataaacatta	acccgagggga	gcataagtta	gtcagacttt	cacctgttaa	gttatggcag	1980
gagaaacaag	tgttttctca	aatgagacaa	cagaaatggt	aaatgatcca	cgtacaaaaa	2040
tcctattagt	tgtactcggt	agagaccgtc	acttgcaagt	ctctagacct	tccctgctag	2100
gtcgaccaac	agacgagcag	aaacagattc	ctcccgaat	ctgaacacat	atttgaacac	2160
aggacaggta	tggcaagggt	cctggctctg	cttgcttagg	tccctgggaa	tcagatcttg	2220
ggtggctgat	gggctttata	aggttttcac	aaacaatctg	ctgtgctagg	ttctcaaata	2280
tctagtgaga	atgggagatt	tttatacatg	gaagcatctc	tcctctctct	ctcctctctc	2340
ctctctcttc	tctctctctc	tctctctctc	tctctctctc	tctctctctc	tctctctctc	2400
ctccctccct	ccctctctct	ctctttgtgt	gcgtgtgtgg	tggggatgag	gacacgtgta	2460
gaacttcggg	ggttgagact	tagtgcatat	gcatacctcac	cattccagtt	agtgaatggt	2520
aacactattt	aaggtcacag	acctaacagc	cttctgtgtc	cggattcctg	gattcctagg	2580
acctttgtgg	atggggttgc	acaccctctg	tgttcatact	gactgtgagg	tcgatgggac	2640
atagtaggga	taactttcat	ttggaatctc	tagagatggg	aggtcatcat	gtcatagaat	2700
gttatcacta	atgaccaaga	tagacactca	tgtttaagag	acatcacaag	gtgtatatta	2760
aatatgacat	ggcatataac	ttgtaatgac	acaaaaatat	tctgttacct	acttttctcc	2820
taaaagcttg	ggactctcca	gagttctaaa	tacatgcaaa	cagattattg	tgttttacag	2880
gaatcttata	ttgaactttc	tttacctgac	tcaaatttta	ttaaaattaa	ctgggaacaa	2940
atagttggtc	tctaattctc	acaaaaacca	ccaaatgatt	acactgagca	taattataat	3000
caccctgctg	ctacgtctag	aaaccaaact	gtgaaatatt	ggctgactgt	ataccttctc	3060
aaataataaa	ttcaggataa	cattgccata	ttattggaga	acccccccct	cccttttaaa	3120
actggaatca	ttttatgtca	atctcagggt	aaatacgaat	gggtttcaga	acagtgctgt	3180
gcactgaagg	ctgacattta	gaacatatat	aacgattttc	gtaaagtctg	ctgtaacaat	3240

tgctgattgt atcctaggag acttggactc ctctcaacgt taaggcagag gaatataatg 3300
gttatgagag taaaactctc tgtcaggtag atctggcttt ctgtcccagc tctgtcactt 3360
aacacttagt tgcggtggga aaactccctg atcttccggg agactaagta actgtataag 3420
caagctggcc gtgatatcca cgtcgttaagg ctgctgtgtg ggttcagtga aaactgttac 3480
agtgattggc agagtttctg gaggtcattg accctcatta aaccttgcat acacttattc 3540
ttactactct ttgctgtag tgttgccacc aggattgcca ttcaaggcag tctgtatac 3600
ttgataacac cagttgggtc tgaggcctta gttagcatct gttagcctgg ttcaggagag 3660
tgtatcagag ccaggttctc ctatcacata aactgtaacg caagtgaatt gtccaattgc 3720
tgttgagtct gagagtcctt gaggtgcata gctttgacta ataaatcccc atgcttttat 3780
gcttttctct cctccctctt ccagttcaac atctaataa caaagattgt tccgaccact 3840
acgtgctagg aaggagaagc agtggggcct acagagttac ccctgatcac agaaacagca 3900
gctttgaggt ctactgtgac atggagacca tgggtggagg ctggacggtg ctgcaggctc 3960
gccttgatgg cagcaccaac ttcaccagag agtggaaaga ctacaaagcc ggctttggaa 4020
accttgaacg agaatttttg ttgggcaacg ataaaattca tcttctgacc aagagtaagg 4080
aaatgatttt gagaatagat cttgaagact ttaatggtct cacactttat gccttgtagt 4140
atcagtttta tgtggctaata gaatttctca aataccgatt acacatcggt aactacaatg 4200
gcacggcagg ggatgccttg cgtttcagtc gacactacaa ccatgacctg aggtttttca 4260
caacccaga cagagacaac gatcggtacc cctctgggaa ctgtgggctc tattacagct 4320
caggctgggtg gtttgattca tgtctctctg ccaattttaa tggcaaata taccaccaga 4380
aatacaaagg tgtccgtaata gggattttct ggggcacctg gcctggtata aaccaggcac 4440
agccagggtg ctacaagtcc tcttcaaac aggccaaagat gatgattagg cccaagaatt 4500
tcaagccata aattgctagt gttcatctct ctgggcactc actatctaag aggacgatga 4560
attccttcag ccttttacca tatgtctcag tttatattcc tttcctatgg ctaaacattt 4620
cctttaaagc tttacagctt ttagaataaa gctgaaaaga tctaaaaaga ctctatggt 4680
gctgttatat gaggaatgct tgaaagcact ggaaatattg acaattatac attataattg 4740
caaaaccttt catttttatt agttgaaaag tttcctaata tttttattat ttttataata 4800
aaaactaaat tattcagcaa gctagattct atatacgcaa gttttatttt cactagggct 4860
aaatatacac atttgagaat ataccagtcc ttccaggtag aactgaaagc caagaactgt 4920
agtattatct ttcgtctaag aagaacttaa agcatttttag ttctcaagaa gaagggcagg 4980
gatgggattg ggggccaggg acaatatgta tagctaaatg tattcatcta atgcaaaaata 5040
tggcattaaa atacctaaaa atgtggtagc ataatatatg tctcttccct ctccaattga 5100
aaaataatgt taccctgtag actttgggtt agtggttaatt cacttactgt ttatagcctg 5160

<210> 4

<212> PRT

<213> Murine fql2

<400> 4

Met Arg Leu Pro Gly Trp Leu Trp Leu Ser Ser Ala Val Leu Ala Ala
1 5 10 15

Cys Arg Ala Val Glu Glu His Asn Leu Thr Glu Gly Leu Glu Asp Ala
20 25 30

Ser Ala Gln Ala Ala Cys Pro Ala Arg Leu Glu Gly Ser Gly Arg Cys
35 40 45

Glu Gly Ser Gln Cys Pro Phe Gln Leu Thr Leu Pro Thr Leu Thr Ile
50 55 60

Gln Leu Pro Arg Gln Leu Gly Ser Met Glu Glu Val Leu Lys Glu Val
65 70 75 80

Arg Thr Leu Lys Glu Ala Val Asp Ser Leu Lys Lys Ser Cys Gln Asp
85 90 95

Cys Lys Leu Gln Ala Asp Asp His Arg Asp Pro Gly Gly Asn Gly Gly
100 105 110

Asn Gly Ala Glu Thr Ala Glu Asp Ser Arg Val Gln Glu Leu Glu Ser
115 120 125

Gln Val Asn Lys Leu Ser Ser Glu Leu Lys Asn Ala Lys Asp Gln Ile
130 135 140

Gln Gly Leu Gln Gly Arg Leu Glu Thr Leu His Leu Val Asn Met Asn
145 150 155 160

Gly Thr Trp Pro Gly Ile Asn Gln Ala Gln Pro Gly Gly Tyr Lys Ser
405 410 415

Ser Phe Lys Gln Ala Lys Met Met Ile Arg Pro Lys Asn Phe Lys Pro
420 425 430

<210> 5

<211> 592

<212> DNA

<213> Murine

<400> 5

atgaggcttc ctggttggtt gtggctgagt tctgccgtcc tcgttgctg cggagcgggtg 60
gaggagcaca acctgactga ggggctggag gatgccagcg cccaggctgc ctgccccgcg 120
aggctggagg gcagcgggag gtgcgagggg agccagtgcc ccttcagct caccctgccc 180
acgctgacca tccagctccc gcggcagctt ggagcatgg aggaggtgct caaagaagtg 240
cggaccctca aggaagcagt ggacagtctg aagaaatcct gccaggactg taagttgcag 300
gctgacgacc atcgagatcc cggcggaat ggagggaaat gagcagagac agccgaggac 360
agtagagtcc aggaactgga gagtcaggtg aacaagctgt cctcagagct gaagaatgca 420
aaggaccaga tccaggggct gcaggggagc ctggagacgc tccatctggt aaatatgaac 480
aacattgaga actacgtgga caacaaagtg gcaaactctaa ccgttggtggt caacagtttg 540
gatggcaagt gttccaagtg tcccagccaa gaacacatgc agtcacagcc gg 592

<210> 6

<211> 613

<212> DNA

<213> Homo sapiens

<400> 6

atgaagctgg ctaactggta ctggctgagc tcagctgttc ttgccactta cggttttttg 60
gttgtggcaa acaatgaaac agaggaaatt aaagatgaaa gagcaaagga tgtctgcccc 120
gtgagactag aaagcagagg gaaatgcgaa gaggcagggg agtgccccta ccaggtaagc 180
ctgccccctt tgactattca gctccgaag caattcagca ggatcgagga ggtgttcaaa 240
gaagtccaaa acctcaagga aatcgtaaata agtctaaaga aatcttgcca agactgcaag 300
ctgcaggctg atgacaacgg agaccaggc agaaacggac tggtgttacc cagtacagga 360
gccccgggag aggttggtga taacagagtt agagaattag agagtgaggt taacaagctg 420

<210> 7

<212> DNA

<213> Murine

<400> 7

<210> 8

<211> 707

<212> DNA

<213> Homo sapiens

<400> 8

ttcaacatct	aatatataaa	gattgctctg	actactacgc	aataggcaaa	agaagcagtg	60
agacctacag	agttacacct	gatcccaaaa	atagtagctt	tgaagtttac	tgtgacatgg	120
agaccatggg	gggaggctgg	acagtgtctg	aggcacgtct	cgatggggagc	accaacttca	180
ccagaacatg	gcaagactac	aaagcaggct	ttggaaacct	cagaagggaa	ttttggctgg	240

<210> 9

<212> DNA

<220>

 $\langle 222 \rangle \quad (384) \dots (384)$

<220>

 $\langle 222 \rangle \quad (468) \dots (468)$ $\langle 220 \rangle$ $\langle 222 \rangle \quad (470) \dots (470)$

<220>

$\langle 222 \rangle$ (505) .. (505)

$\langle 220 \rangle$

<222> (524) .. (524)

<220>

 $\langle 222 \rangle \quad (668) \dots (668)$

<223> n is any nucleic acid

<400>	9						
atcactctgt	tcattcctcc	aggtattcgt	tatctaatag	ggcaattaat	tccttcagca		60
ctttagaata	tgccttgttt	catatttttc	atagctaaaa	aatgccttgt	ttcatatttt		120
tcatagctaa	aaaatgatgt	ctgacggcta	ggttcttatg	ctacacagca	tttgaaataa		180
agctgaaaaa	caatgcattt	taaaggagtc	ctttgttggt	atgctgttat	ccaatgaaca		240
cttgcaagca	attagcaata	ttgagaatta	tacattagat	ttacaattct	tttaatttct		300
attgaaactt	tttctattgc	ttgtattact	tgctgtatgt	aaaaaataat	tgttggtcgg		360
gtgtggtagc	tcacgcctgt	aatnccagca	ctttggaatg	tcaaggcagg	cagatcactt		420
gaggtcagga	gtttgagacc	agcctggcca	aacatgtgaa	acgctgtntn	tattaaanaat		480
acaaaaatta	gccgggcatg	gtggnacatg	cctgtaatcc	tagntacttg	ggaggcctgag		540
gcaggagaat	cgcttgaacc	tgagaggaag	aggttgcagt	gagccaagaa	tgagccactg		600
cactccagca	tgggtgacag	agaaaaactct	gtctcaaaca	aaaaaataat	aaaattttatt		660
cagtaggntg	gattctacac	aaagtaatct	gtatttgggc	catgatttaa	gcacatctga		720
aggtatatca	ctcttttcag	gctataatta	tttgggtaat	cttcattctg	agacaaaactt		780
aatctatatc	atttactttg	caacagaaca	accctacagc	attttggttc	ccagactaag		840
ggaactaata	totatataat	taaacttggt	cattttatcat	tcatgaaata	taaaataactt		900
gtcattttaa	ccgttttaaa	atgtggtagc	ataatgtcac	cccaaaaagc	attcagaaag		960
caatgtaact	gtgaagacca	gggttttaaag	gtaattcatt	tatagtttat	aactccttag		1020
atgtttgatg	ttgaaaactg	ctttaacatg	aa				1052

<210> 10

<211> 1339

<212> DNA

<213> Murine

<400> 10

```
tcgggtttgga tatcatggga tggaatgaga agggaaagta ggagcccgag agtgcggtaa      60
gacaaggcat aaggcgtgtc tgacaaattc ttcatacaca catttcccct ttgcacattc      120
agtctgtata ggttatttct ataggagaaa aaaaatattc aaattccttg tgcactggta      180
acaggcatga aggctcagca aagccaatac gtgttatgtc cagttggaga cagtgccagg      240
gccaacattc cagacttctc agatagaaag tgcgcctgcc tgccctgctc tgagaatttg      300
aagagagtag ttcagttaga attaagaggc agtagagaaa agtcttggga aatctggtta      360
gagatataaa tatgagaact ggacatggtg gtacacacct gtgatctctg tgtttaggag      420
ggagaggcag agagatcagg agttcaaggc cagcctgagc tacttgagac ccagtctaaa      480
taaataagag atagattaca gagtgccttt aactagtaca gagaaagaat ttgggtttat      540
ctgtgtcagt tacgctgaaa taatttttaa gtaataaaat cccttttaat aagaaacctt      600
atgaggtcag tatgcacaat gaacttaaga gagaccccca gctcctgagc tgagtgatgg      660
ggaaggacag ccactgcctg tgatgtgtga gtgacgtgct tccaagtgtt ttaaccactg      720
acgattacat agcctgcaca gtcaggagaa aacagccgta ttctctgcca gttctcttcc      780
cttttacaaa cagatgagag acacacacag agaatccatt taaagagcgg acctttgttc      840
tgattagggg caatttttaag tacttaagag ttcacacaaa gtctagcctt caaaaagaaa      900
acaggttccc aaactaggga ggaaacagaa tcatttccat tttggtgaca tttagtggga      960
agaagctcac agacatttag acgttccaac tctttcccca ctagtggacc aagtatataa     1020
tatggtatct tttgggcact ggtattacaa ctgtttttta aacaaaagac tttccttgtg     1080
ctttactaaa aaccagacg gtgaatcttg aatacaatgc gtggcaccca cggcaggcat     1140
tctattgtgc atagttttga ctgacaggag atgacagcat ttggctggct gcgcttgctg     1200
aggaccctct cctcctgtgt ggcgctctgag actgtgatgc aaatgcgccc gcccttttct     1260
gggaactcag aacgcctgag tcaggcggcg gtggctatta aagcgcttgg tcaggctggg     1320
ctgccgcact gcaaggatg                                     1339
```

<210> 11

<211> 1338

<212> DNA

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted October 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

<213> Homo sapiens

```

<400> 12
tagggttgga agccaggtct cctgagtatg cgagaataaa tacagtcatg gaagtgtaaa      60
gagtctgcca acatttttgag aatgtgaata ggatttggct aaaattaagg ggatatacag      120
aaaagtcata ggaaatcagg ttaaagacat aaatatgaga taggctacag agtgtttttaa      180
gtaatacaat aaaacattta gatttttgcc catgtcagtc attttgaaat tattttttaa      240
gcaaaaaaac cttttttaa caagaaatct tatgagatgt caatatgcaa aacaaattaa      300
aaggaggtgg tttctctaac tgaagctgtt cctctttcct gccttcagcc tctgaagaga      360
aagttagaaa actattatca ttaatgctac atgttttgaa caagctgata taccaagtgg      420
cccagagagc aggtagaaga accagcgtgg agacagaaag caagaggccc gcctgccagg      480
gctacctgca gaaagaaagg gcaaagatgc tgtaggcaag agaagttcag gacagacact      540
ggcatagctc aaagattcac atttgagcag ctgtggaaga tgacagtaca attaccaaaa      600
tgtcgaaggg caaaggaggc agctactggt tttgatgaaa gacaattatg tcctttttaa      660
tgggtcttag acatttagac atttatatac actatgctac ggacaaagga atagaaagta      720
gcactttttt ctccactagt tttcttctct ttttcaagta gatgaagcaa aagtcaactg      780
ccaatagtca gaaagctgta ctttgttaca cttagaaact tctaaaagtg ctttaagattt      840
cacctgaaac gccaacatga agaaaataca ggctcccaa tgccccattc taagaagaaa      900
aaggaccatt ttcatttttag taacgtttct gttctataga cagtttggat aactagctct      960
tactttttat ctttaaaaac tgtttttcca gtgaagttac gtataattat ttacttcaag     1020
cgtagtatac caaattactt tagaaatgca agacttttct tatacttcat aaaatacatt     1080
atgaaagtga atcttgttgg ctgtgtacat ttgactataa taatttcaat gcatattatt     1140
tctattgaga gtaagttaca gtttttggca aactgcgttt gatgaggggt atctcctctt     1200
cctgtgcgtt tctaaaactt gtgatgcaaa cgctcccacc ctttcctggg aacacagaaa     1260
cgctactcag gcacgtgccg gtattaaagc agctccagcc ctgcgcactc cctgctgggt     1320
gagcagcact gtaaagatg                                           1339

```

<210> 13

<211> 328

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (265)..(265)

```
<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence
```

<223> Primer

gcaaacaatg aaacagagga aa

22

<210> 17

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 17

attgccctat tagataacga atac

24

<210> 18

<211> 15

<212> PRT

<213> Homo sapiens

<400> 18

Asp Arg Tyr Pro Ser Gly Asn Cys Gly Leu Tyr Tyr Ser Ser Gly
1 5 10 15

<210> 19

<211> 7

<212> DNA

<213> Artificial Sequence

<220>

<223> API motif

 $\langle 220 \rangle$

```
<221> misc_feature
```

$$\langle 222 \rangle \quad (4) \dots (4)$$

<210> 23

<211> 21

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Primer

<400> 23

gggcactggt attacaactg t

21

<210> 24

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 24

ctcctcctgt gtggcgctctg a

21

<210> 25

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 25

ggataaggag ggcaggggtga a

21

<210> 26

<211> 21

<212> DNA

<213> Artificial Sequence

<223> Primer

acagttgtaa taccagtgcc c

21

<211> 21

<212> DNA

<213> Artificial Sequence

<223> Primer

aacggagacc caggcagaaa c

21

<211> 21

<212> DNA

<213> Artificial Sequence

<223> Primer

cttcgggagc tgaatagtca a

21

<210> 29

<211> 21

<212> DNA

<213> Artificial Sequence

<223> Primer

gacagcaaag tggcaaact a

21

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 30
ttctggtgaa gttggtgctc c

21

<210> 31
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 31
caaaagaagc agtgagacct aca

23

<210> 32
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 32
tgaccaagag taaggaaatg a

21

<210> 33
<211> 22
<212> DNA
<213> Artificial Sequence

Sequence

17

<213> Artificial Sequence

19

<213> Artificial Sequence

20

<213> Artificial Sequence

19

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 44
aaggcaggaa agaggaac

18

<210> 45
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 45
gacaaaggaa tagaaagtag c

21

<210> 46
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 46
cagggcaaaa atctaaatg

19

<210> 47
<211> 19
<212> DNA
<213> Artificial Sequence

$\langle 220 \rangle$

<223> Primer

<400> 47

gccagagag caggtagaa

19

<210> 48

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 48

ccagccaggg ttgaaata

18

<210> 49

<211> 18

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Primer

<400> 49

gccctgtcag tcattttg

18

<210> 50

<211> 19

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Primer

<400> 50

aaaaacctac cagtagtct

19

<210> 51
<211> 17
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 51
ttggggtgac attatgc

17

<210> 52
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 52
tgagcagcac tgtaaagatg

20

<210> 53
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 53
gtggcttaaa gtgcttggt

20